Delaval, Jan

46767

From: Sent: To: Subject:

Roark, Jessica Monday, July 16, 2001 7:25 AM Delaval, Jan 09/484577

Good Morning Jan,

Please search from 09/484577

SEQ ID NO:3.

Please include interference.

Results on paper.

Thanks!

Jessica H. Roark

CM1 9B03 Mailbox 9E12 Art Unit 1644 703 605-1209

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Post-processing: Minimum Match 0% Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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AJ391260 Neisseria AE002524 Neisseria	AE004049 Xylella f AJ391263 Neisseria AF121772 Neisseria	AR068625 Sequence	U51197 Sphingomona	AF273216 Rhizobium	Description	

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                                                                                                                                                                       Submitted (30-MAY-2000) Biological Sciences, Un 2500 University Drive NW, Calgary, AB T2N 1N4,
                                                                                                                                                                                                                2 (bases 1 to 3526)
Venter, A.P., Twelker
Direct Submission
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hter,A.P., Twelker,S. and Hynes,M.F.
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/strain="306"
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                                            /clone="pRle306c"
                                                                /db_xref="taxon:387"
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    caaaccgtcaaggccggcgagattctgatcgagctggatccattcgcgggtggtgtgtat 364
                                              GTCAAGGTGATCCAGTCGAGGTTGGCAAGACGATCGCGGTTCCGGTCTCGAACGGT
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                                                                                                                                    TATATCGGCACGTTCGATATCGTGGCGACCGCTCAGGGCAAGATCCAGCCGACCGGGCGC
                                                                                                                                                                          ggtctcggcaggatcgacatcgttgcttctgcatccagaaagatcgtgccgggcgaccgt
                                                                                                                                                                                                                         ATCCGCACGGCGCTCATCTGGTTCATCTGCCTGTTCACAGCCGGCGCACTGATCTGGAGC 2521
                                                                                                                                                                                                                                                        accgcgagactcacggccgccttgcttgctgccttgttctactgcgccgtggcgtgggcg 184
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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114HRLATVRHUNRIIGMKDGRIVEEGTHETLLARPNGLYAHLMQLQTGFIES"
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GGIKAIKTTVADNAEKQAAASSEIDEKEQQLVKAAKKILESMTIKSPINGIVQTSAITT
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2348. .>
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em_esthum10:*
em_esthum11:*
em_esthum12:*
em_esthum13:*

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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gb_est7:*
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em_esthum8:*
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em_esthum1:*
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                                                                        em_esthum3:*
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9b_est29:
9b_est30:
9b_est310:
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em_estpl9:*

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9b_est48: *
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9b_est52: *
9b_est55: *
9b_est56: *
9b_est56: *
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9b_est60: *
9b_est
     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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gb_est111:*
gb_htc:*
                                                                                                           em_gss_vrt2:*
em_gss_vrt3:*
gb_gss1:*
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em_gss_hum1:*
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Result

No.

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RESULT 1
CNS0070E/c
                                   REFERENCE
                                                                                                     SOURCE
ORGANISM
                                                                                                                                     KEYWORDS
                                                                                                                                                                       ACCESSION
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   AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                            Score
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Direct Submission
                 Genoscope
                                                                                              Drosophila melanogaster
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AIR81920 606075806
AL101589 Drosophil
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BE604637 WHE1413-1
BE585055 5-7F-ZO P
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BG314210 WHE2460_F
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Genoscope.

Direct Submission

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genome survey sequence TET3 end of BAC #BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL053013
                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                       Drosophila melanogaster
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                                                                                                                                          (bases 1 to 925)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14D21"
/note="end : TET3"
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                                                                                                                                                                                                                                                                                                                                                                                                                     385 catcacggtgtcggcgcccacgga 409
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcoyo Osoegawa and maron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
               EST.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                         AV630811 508 bp mRNA EST 15-DEC-2000 AV630811 Chlamydomonas reinhardtii 5% to 0.04% CO2 Chlamydomonas reinhardtii cDNA clone LCL084f07_r 5', mRNA sequence.
AV630811
AV630811.1 GI:10793445
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(bases 1 to 508)
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/db_xref="taxon:7227"
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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                                                                                                                                                                                                                          1 (bases 1 to 772)
Wong,R.M.-Y. Wong,K.K., Benson,N.R. and McClelland,M.
Sample sequencing of a Salmonella typhimurium LT2 lambda library:
comparison to the Escherichia coli K12 genome
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AF075872 Salmonella t
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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                                                   Sidney Kimmel Cancer Center
3099 Science Park Road, San Diego
Email: mcclellandelifsci.sdsu.edu
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                               Class: shotgun
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                                                                                                                                                         Contact: McClelland M
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/clone_lib="Chlamydomonas reinhardtii 5% to 0.04% CO2"
/clone_lib="Chlamydomonas reinhardtii 5% to 0.04% CO2"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
/note="The cONA library was constructed from cells cultured in a carbon stress acclimatized condition in which carbon
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genomic clone 142-T3, DNA sequence.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Human adenosine Al	Mycobacteriophage	Thermus thermophil	T. thermophilus on			cDNA clone pf7 enc	Mycobacterium tube		Wheat Nph2-2 prote	Pse	GD.	Pseudomonas sp. WF			HSV-2 strain SB5 C	Complete nucleotid	que		Zea mays DNA fragm	Streptomyces nogal	Corn sulphate perm	C. acidivorans gam	Nucleotide sequenc	Streptomyces prist	Streptomyces prist	Gene encoding a su			Streptomyces freno	റ		₹D	A. pleuropneumonia

ALIGNMENTS

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/codon_start= 70767078	B	CT I	∄ ,[,	∄ - 10	Sphinomonas strain S88 (ATCC 31554). Key Location/Qualifiers CDS complement (19421944) /*tag= a	Sphingan biosynthetic gene region. Sphingan; polysaccharide; spsB gene; glucosyl-IP-transferase; ds	AAT37329;	T 1 329/c AAT37329 standard; DNA; 28804 BP.

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24113..24115
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16748..16750
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15883..15885
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/note= "spsD gene putative
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complement (27534..27536)
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/note= "rhsC gene putative
24683..24685
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/note= "urf34
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/product= glu
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/note= "urf31 gene putative"
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/note= "rhs8 gene putative initiation codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A 28.8 kb chromosomal fragment of Sphingomonas strain S88 was isolated on the basis of its ability to restore sphingan biosynthetic capability to Sphingomonas mutant S88m260. It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated DNA from Sphingomonas sp. - used for transforming recipient bacteria to obtain hyper-producers of sphingan \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28804 BP; 4974 A; 9806 C; 9228 G; 4796 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 32; Page 56-70; 105pp; English
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(SHIE ) SHINETSU CHEM CO LTD.
                                                                                                    Sphingomonas genus microbe isolated DNA sequence producing sphingan.
                                                                                                                                                                                                     AAT92474 standard; DNA; 28804 BP
                            Sphingomonas sp.
                                                           sphingan S-88; spsB gene;
                                                                        Sphingomonas microbe; sphingan polysaccharide biosynthesis gene;
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INCREASING		19, 19, 19, 22, 22, 20, 20, 20, 20, 20, 20, 20, 20	Sequence 11, Appl Sequence 10, Appl Sequence 10, Appl Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 4, Appli Sequence 4, Appli Sequence 3, Appli

Query Match

17.7%;

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SOFTWARE: PatentIn Ver. 2.0
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CURRENT FILING DATE: 1998-06-12
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APPLICANT: Mikolajczak, Marcia
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                                                                                   TCCCCCGAAAGCGGTATCGTCCGGCGCATTCTGGTGGGCGAGGGGCCAGAAGGTTCAGAAG 18569
                                                                                                                                                                      GAAGTGGTGGCGCCGACGCAGGGCCGCATCGCCCCGATCGGCGAGACCAAGATCGTGCAG 18629
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Pred. No. 1.1e-14;
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; ORGANISM: Sphingomonas sp.
US-09-096-867-2
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APPLICANT: POLLOCK, Thomas J

APPLICANT: Mikolajczak, Marcia

APPLICANT: Yamazaki, Motohide
                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2
LENGTH: 28804
                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application Patent No. 6019984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: MacInn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 1998-06-11
EARLIER APPLICATION NUMBER: 60/049,428
EARLIER FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Production of Xanthan Gum by Sphingomonas Bacteria TITLE OF INVENTION: Carrying Genes from Xanthomonas Campestris FILE REFERENCE: seq list for appl filed from pro. appl CURRENT APPLICATION NUMBER: US/09/096,867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Thorne, Linda
APPLICANT: Armentrout, Richard W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
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COMPUTER READABLE FORM:
                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                     APPLICANT:
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                                       COUNTRY:
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les 165; Conserv
                                                                                                                        ADDRESSEE:
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                                                                              Toronto
                                                             Ontario
                                                                                                  40 King Street
                                       Canada
                                                                                                                                                                                                                               Rosendal,
                                                                                                                                                                                                                                                     Mallard, Bonnie
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                                                                                                       Bereskin & Parr
King Street West
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56.5%;
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NOVEL BACTERIAL PREPARATIONS,
PRODUICING SAME, AND THEIR USE
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